RAW SEQUENCE LISTING   DATE: 04/30/2003
PATENT APPLICATION: US/09/674,817B   TIME: 11:33:05

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Output Set: **N:\CRF4\04302003\I674817B.raw**

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   3 <110> APPLICANT: Hoechst Schering AgrEvo GmbH
   4       LTRZ, Horst
   5       LsTTICKE, Stephanie
   6       ABEL, Gernot
   7       GENSCHEL, Ulrich
   9 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES WHICH CODE FOR ENZYMES DERIVED FROM
WHEAT AND
  10       WHICH ARE INVOLVED IN THE SYNTHESIS OF STARCH
  12 <130> FILE REFERENCE: 514413-3849.1
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/674,817B
C--> 14 <141> CURRENT FILING DATE: 2000-11-06
  14 <150> PRIOR APPLICATION NUMBER: WO 99/58690
  15 <151> PRIOR FILING DATE: 1999-11-18
  17 <150> PRIOR APPLICATION NUMBER: DE 198 20 608.9
  18 <151> PRIOR FILING DATE: 1998-05-08
  20 <150> PRIOR APPLICATION NUMBER: 09/674,817
  21 <151> PRIOR FILING DATE: 2000-11-06
  23 <160> NUMBER OF SEQ ID NOS: 11
  25 <170> SOFTWARE: PatentIn version 3.1
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  55 gcg ggg aag ggg gtc ggc gag gtg tgc gcc gcg gtt gtc gag gcg gcg         95
  56 Ala Gly Lys Gly Val Gly Glu Val Cys Ala Ala Val Val Glu Ala Ala
  57                  20                  25                  30
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  60 Thr Lys Val Glu Asp Glu Gly Glu Glu Asp Glu Pro Val Ala Glu Asp
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65          50                55                60
67 ccg ctg ggc gcc acc gcg ctc gcc ggc ggg gtc aat ttc gcc gtc tat        239
68 Pro Leu Gly Ala Thr Ala Leu Ala Gly Gly Val Asn Phe Ala Val Tyr
69          65                70                75
71 tcc ggc gga gcc acc gcc gcg gcg ctc tgc ctc ttc acg cca gaa gat        287
72 Ser Gly Gly Ala Thr Ala Ala Ala Leu Cys Leu Phe Thr Pro Glu Asp
73 80                85                90                95
75 ctc aag gcg gtggggttgc ctcccgagta gagttcatca gctttgcgtg               336
76 Leu Lys Ala
79 cgccgcgcgc cccttttttg ggcctgcaat ttaagttttg tactggggca aatgctgcag     396
81 gat agg gtg acc gag gag gtt ccc ctt gac ccc ctg atg aat cgg acc        444
82 Asp Arg Val Thr Glu Glu Val Pro Leu Asp Pro Leu Met Asn Arg Thr
83     100               105               110
85 ggg aac gtg tgg cat gtc ttc atc gaa ggc gag ctg cac aac atg ctt        492
86 Gly Asn Val Trp His Val Phe Ile Glu Gly Glu Leu His Asn Met Leu
87 115               120               125               130
89 tac ggg tac agg ttc gac ggc acc ttt gct cct cac tgc ggg cac tac        540
90 Tyr Gly Tyr Arg Phe Asp Gly Thr Phe Ala Pro His Cys Gly His Tyr
91              135               140               145
93 ctt gat gtt tcc aat gtc gtg gtg gat cct tat gct aag gca gtg ata        588
94 Leu Asp Val Ser Asn Val Val Val Asp Pro Tyr Ala Lys Ala Val Ile
95          150               155               160
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98 Ser Arg Gly Glu Tyr Gly Val Pro Ala Arg Gly Asn Asn Cys Trp Pro
99          165               170               175
101 cag atg gct ggc atg atc cct ctt cca tat agc acg ttt gat tgg gaa       684
102 Gln Met Ala Gly Met Ile Pro Leu Pro Tyr Ser Thr Phe Asp Trp Glu
103     180               185               190
105 ggc gac cta cct cta aga tat cct caa aag gac ctg gta ata tat gag       732
106 Gly Asp Leu Pro Leu Arg Tyr Pro Gln Lys Asp Leu Val Ile Tyr Glu
107 195               200               205               210
109 atg cac ttg cgt gga ttc acg aag cat gat tca agc aat gta gaa cat       780
110 Met His Leu Arg Gly Phe Thr Lys His Asp Ser Ser Asn Val Glu His
111              215               220               225
113 ccg ggt act ttc att gga gct gtg tcg aag ctt gac tat ttg aag gag       828
114 Pro Gly Thr Phe Ile Gly Ala Val Ser Lys Leu Asp Tyr Leu Lys Glu
115              230               235               240
117 ctt gga gtt aat tgt att gaa tta atg ccc tgc cat gag ttc aac gag       876
118 Leu Gly Val Asn Cys Ile Glu Leu Met Pro Cys His Glu Phe Asn Glu
119          245               250               255
121 ctg gag tac tca acc tct tct tcc aag atg aac ttt tgg gga tat tct       924
122 Leu Glu Tyr Ser Thr Ser Ser Ser Lys Met Asn Phe Trp Gly Tyr Ser
123     260               265               270
125 acc ata aac ttc ttt tca cca atg aca aga tac aca tca ggc ggg ata       972
126 Thr Ile Asn Phe Phe Ser Pro Met Thr Arg Tyr Thr Ser Gly Gly Ile
127 275               280               285               290
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133 gag gct cac aaa cgg gga att gag gtg atc ctg gat gtt gtc ttc aac    1068
134 Glu Ala His Lys Arg Gly Ile Glu Val Ile Leu Asp Val Val Phe Asn
135             310             315             320
137 cat aca gct gag ggt aat gag aat ggt cca ata tta tca ttt aag ggg    1116
138 His Thr Ala Glu Gly Asn Glu Asn Gly Pro Ile Leu Ser Phe Lys Gly
139             325             330             335
141 gtc gat aat act aca tac tat atg ctt gca ccc aag gga gag ttt tat    1164
142 Val Asp Asn Thr Thr Tyr Tyr Met Leu Ala Pro Lys Gly Glu Phe Tyr
143         340             345             350
145 aac tat tct ggc tgt ggg aat acc ttc aac tgt aat cat cct gtg gtt    1212
146 Asn Tyr Ser Gly Cys Gly Asn Thr Phe Asn Cys Asn His Pro Val Val
147 355             360             365             370
149 cgt caa ttc att gta gat tgt tta aga tac tgg gtg acg gaa atg cat    1260
150 Arg Gln Phe Ile Val Asp Cys Leu Arg Tyr Trp Val Thr Glu Met His
151             375             380             385
153 gtt gat ggt ttt cgt ttt gat ctt gca tcc ata atg acc aga ggt tcc  · 1308
154 Val Asp Gly Phe Arg Phe Asp Leu Ala Ser Ile Met Thr Arg Gly Ser
155             390             395             400
157 agt ctg tgg gat cca gtt aac gtg tat gga gct cca ata gaa ggt gac    1356
158 Ser Leu Trp Asp Pro Val Asn Val Tyr Gly Ala Pro Ile Glu Gly Asp
159             405             410             415
161 atg atc aca aca ggg aca cct ctt gtt act cca cca ctt att gac atg    1404
162 Met Ile Thr Thr Gly Thr Pro Leu Val Thr Pro Pro Leu Ile Asp Met
163         420             425             430
165 atc agc aat gac cca att ctt gga ggc gtc aag ctc att gct gaa gca    1452
166 Ile Ser Asn Asp Pro Ile Leu Gly Gly Val Lys Leu Ile Ala Glu Ala
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169 tgg gat gca gga ggc ctc tat caa gta ggt caa ttc cct cac tgg aat    1500
170 Trp Asp Ala Gly Gly Leu Tyr Gln Val Gly Gln Phe Pro His Trp Asn
171             455             460             465
173 gtt tgg tct gag tgg aat ggg aag tac cgg gac att gtg cgt caa ttc    1548
174 Val Trp Ser Glu Trp Asn Gly Lys Tyr Arg Asp Ile Val Arg Gln Phe
175             470             475             480
177 att aaa ggc act gat gga ttt gct ggt ggt ttt gcc gaa tgt ctt tgt    1596
178 Ile Lys Gly Thr Asp Gly Phe Ala Gly Gly Phe Ala Glu Cys Leu Cys
179             485             490             495
181 gga agt cca cac cta tac cag gtaagttgtg·gcaatacttg taaatgagtt      1647
182 Gly Ser Pro His Leu Tyr Gln
183         500             505
185 gagtgaatgt cacctggatt ttttatatat accacatgat gatacacatc taaatatata 1707
187 acaatcatag tgtatgcata tgcatttggc taagaagtat tagtgtatac actagtgcta 1767
189 tatataggtt ttaacaccca acttgccaat gaaggaacat agggctttct agttatctta 1827
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195 tgcttttctg taaagaaagg aaaacgactt catactttct atcggtgcta acttagctcg 2007
197 atgtatattt gtaagatgaa tgccaaattt aatttgtcgg ataatttgat ctgttattca 2067
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202                 Ala Gly Gly Arg Lys Pro Trp His Ser Ile Asn
203                               510                 515
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206 Phe Val Cys Ala His Asp Gly Phe Thr Leu Ala Asp Leu Val Thr Tyr
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209 aat aag aag tac aat tta cca aat ggg gag aac aac aga gat gga gaa      2273
210 Asn Lys Lys Tyr Asn Leu Pro Asn Gly Glu Asn Asn Arg Asp Gly Glu
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213 aat cac aat ctt agc tgg aat tgt ggg gag gaa gga gaa ttc gca aga      2321
214 Asn His Asn Leu Ser Trp Asn Cys Gly Glu Glu Gly Glu Phe Ala Arg
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217 ttg tct gtc aaa aga ttg agg aag agg cag atg cgc aat ttc ttt gtt      2369
218 Leu Ser Val Lys Arg Leu Arg Lys Arg Gln Met Arg Asn Phe Phe Val
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223                 585                 590                 595
225 tat ggc cac aca aaa ggg ggc aac aac aat aca tac tgc cat gat tct      2465
226 Tyr Gly His Thr Lys Gly Gly Asn Asn Asn Thr Tyr Cys His Asp Ser
227             600                 605                 610
229 tat gtc aat tat ttt cgc tgg gat aaa aaa gaa caa tac tct gag ttg      2513
230 Tyr Val Asn Tyr Phe Arg Trp Asp Lys Lys Glu Gln Tyr Ser Glu Leu
231         615                 620                 625
233 cac cga ttc tgc tgc ctc atg acc aaa ttc cgc aag gag tgc gag ggt      2561
234 His Arg Phe Cys Cys Leu Met Thr Lys Phe Arg Lys Glu Cys Glu Gly
235     630                 635                 640
237 ctt ggc ctt gag gac ttt cca acg gcc aaa cgg ctg cag tgg cat ggt      2609
238 Leu Gly Leu Glu Asp Phe Pro Thr Ala Lys Arg Leu Gln Trp His Gly
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242 His Gln Pro Gly Lys Pro Asp Trp Ser Glu Asn Ser Arg Phe Val Ala
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247             680                 685                 690
249 acc agc cac tta ccg gcc gtt gtt gag ctc cca gag cgc gca ggg cgc      2753
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254 Arg Trp Glu Pro Val Val Asp Thr Gly Lys Pro Ala Pro Tyr Asp Phe
255     710                 715                 720
257 ctc acc gac gac tta cct gat cgc gct ctc acc ata cac cag ttc tcg      2849
258 Leu Thr Asp Asp Leu Pro Asp Arg Ala Leu Thr Ile His Gln Phe Ser
259 725                 730                 735                 740
261 cat ttc ctc tac tcc aac ctc tac ccc atg ctc agc tac tca tcg gtc      2897
262 His Phe Leu Tyr Ser Asn Leu Tyr Pro Met Leu Ser Tyr Ser Ser Val
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Input Set : **N:\vernette\09674817b.raw.TXT**
Output Set: **N:\CRF4\04302003\I674817B.raw**

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284 aggacgagcc ggtggcggag gacaggtacg cgctcggcgg cgcgtgcagg gtgctcgccg    180
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352 cttggcacag tatcaacttt gtatgtgcac atgatggatt tacactggct gatttggtaa   2220
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VERIFICATION SUMMARY   DATE: 04/30/2003
PATENT APPLICATION: **US/09/674,817B**   TIME: 11:33:06

Input Set : **N:\vernette\09674817b.raw.TXT**
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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:44 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:35
L:50 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:41
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